

RESEARCH ARTICLE

White Blood Cell Classification Using Convolutional Neural Network

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HIGHLIGHTS

- A CNN based model with low number of trainable parameters for classification of white blood cell types has been provided.
- The proposed model's performance assessed using several optimizers such as RMSprop, Adam, and Adagrad.
- We have compared four pre-trained models such as MobileNetV2, DenseNet121, InceptionV3 and ResNet50 with our proposed model.

Keywords:

- White blood cells
- Blood Cell Classification
- CNN
- DenseNet121

GRAPHICAL ABSTRACT

Unlike other studies, this paper provides a CNN based model with low number of trainable parameters for classification of white blood cell types. This model is made up of five convolution blocks, which are responsible for extracting the features, flatten layer, fully connected layers and a final FC layer with SoftMax activation function. Conv2D is used in the first convolution block, which is the input block, and SeparableConv2D (Separable convolutions) are used in the following convolution blocks. The proposed CNN model is shown in the below figure.



Figure. Proposed CNN model.

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Aim of Article: The key purpose of this study is to provide a CNN based model with low number of trainable parameters for processing white blood cells with the aim of classifying the type of these cells.

Theory and Methodology: A Convolutional Neural Network based model has been used in this paper which consists of five convolutional blocks.

Findings and Results: Compared to four pre-trained CNN models, and other related studies our proposed model with the lowest number of trainable parameters and training time shows the great results with 99.5% accuracy, 99% recall, 99% precision, and 99% F1 score.

Conclusion: We achieved the key purpose of this study, by building a CNN-based model with low number of trainable parameters for classification of white blood cell types.



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- The proposed model's performance assessed using several optimizers such as RMSprop, Adam, and Adagrad.
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*Corresponding Author:	classifying white blood cell types and assessed the model's performance using several optimizers. We have seen that the RMSprop optimizer shows the best result in our proposed model. We have		
Shamriz Nahzat <u>shamriz.nahzat19@ogr.atauni.e</u> <u>du.tr</u> +90 552 383 20 41.	compared four pre-trained models such as MobileNetV2, DenseNet121, InceptionV ResNet50 with our proposed model. Compared to four pre-trained CNN models, and other studies, our proposed model with the lowest number of trainable parameters and trainin shows the great results with 99.5% accuracy, 99% recall, 99% precision, and 99% F1 score		

Keywords: White blood cells, Blood Cell Classification, ,CNN, DenseNet121.

I. INTRODUCTION

The use of artificial intelligence (AI) algorithms, machine learning, and, in particular, deep learning methods in different medical and biological applications is quickly rising as the capacity of computer processors increases. These algorithms are utilized in various of disciplines, ranging from automated and semi-automated systems for analyzing medical pictures to big data processing algorithms for processing human genome information [1]. The quantitative and qualitative evaluation and analysis of microscopic images of blood samples is one of the applications of artificial intelligence (AI) in medicine [2]. The goal of microscopic blood sample analysis is to count various cells in blood samples, like red-white blood cells, and platelets, or to assess their quality [3].

In the meantime, since WBCs are a key element of the immune system and demonstrate resistance to a variety of illnesses, quantitative and qualitative examination of various kinds of white blood cells is critical. Counting



white blood cells can help doctors detect and treat illnesses like AIDS and leukemia. As a result, one of the most important steps in analyzing and testing blood samples is counting various types of white blood cells.

Automatic and non-automatic methods can be used to analyze and count different kinds of white blood cells in blood samples. In non-automated methods, a blood sample is taken from a patient and examined by a specialist, in this method the analysis and counting of blood sample cells is a slow, tedious, time-consuming, and will be an inaccurate process. In contrast, there are several automated systems for the quantitative evaluation and WBC classification, based primarily on flowmeters and the chemical properties of the cells. These systems are often expensive and somewhat slow, providing only quantitative information about blood cells [4].

As a result, developing and implementing low-cost, quick, and reliable systems for evaluating, classifying, and counting various kinds of white blood cells is important. Processing microscopic images of blood samples are one of the most frequent approaches for building and implementing these systems.

The main purpose of this study is to implement a CNN based model for processing of WBCs with the aim of classifying the type of these cells. In this study, our focus will be on detecting the type of WBCs in white blood cell images.

Images of Kaggle white blood cells were utilized to do this. The collection contains 12,444 augmented microscopic images of eosinophils, monocytes, lymphocytes, and neutrophils, with almost 3,000 photographs for each of the four cell types [5].

In this article, we built a CNN-based model for classifying white blood cell types and assessed the model's performance using several optimizers such as RMSprop, Adam, and Adagrad. In addition, to evaluate the accuracy of our proposed model, we have been compared with four Pre-trained Keras models such as MobileNetV2, DenseNet121, InceptionV3 and ResNet50. The following is how the rest of the paper is structured: In part 2, we go through a few recent research on the classification of WBC types. The material and method are discussed in Section 3, experimental data from the study's dataset, as well as deep learning approaches, are discussion, whereas

section 5 contains the study's conclusions.

II. RELATED WORKS

This part of the paper is allocated to several scholars who have discussed issues relating to white blood cell types classification.

Cheque et al. [6], in 2021, suggested a multi-level and hybrid model for WBC classification. They utilized a Faster R-CNN network in the first stage to identify the region of interest in white blood cells and to separate mononuclear cells from polymorphonuclear cells. After that, they employed two parallel convolutional neural networks with the MobileNet structure, in the second stage to detect WBC subtypes. Their proposed model shows a performance metric of around 98.4% (accuracy, recall, precision, and F1-score) in Kaggle blood cells dataset.

In 2021 Çınar & Tuncer [7] have classified WBC using the CNN Alexnet-Googlenet-SVM hybrid model. In this combined model, the feature vectors of the last pooling layer both architectures are integrated. The properties obtained are classified by the SVM technique. Their model has been tested with Kaggle and LISC datasets, the accuracy of both datasets is 99.73 and 98.23, respectively. The entire number of parameters and trainable parameters that can be utilized to train the developed model is not mentioned in their article.

In 2021 Akiz et al. [8] Classified white blood cells using convolutional features and Support Vector Machines. finally, their proposed model shows 85.95% accuracy.

In 2020, Toğaçar et al. [9] utilized three pre-trained models for feature extractor purposes, including GoogLeNet, AlexNet, and ResNet-50, and used the quadratic discriminant analysis (QDA) classifier to identify white blood cells. As a consequence, they were able to classify different types of WBCs with a 97.95 percent success rate. The accuracy of the model is improved by employing feature selection in the classification step, according to the authors.

In 2019, Özyurt [10] introduced the CNN–MRMR– ELM hybrid model, which used pretrained CNN models such as AlexNet, GoogleNet, VGG-16, and ResNet to extract features. After integrating these features, he selected 400 important features using the MRMR feature selection technique. Then he classified



WBC Image Input

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white blood cells using the ELM algorithm, and his proposed model had an accuracy of 96.0.3 %.

In 2018, Tiwari et al. [11] classified white blood cell types using a CNN-based model, which is a Double Convolution Layer Neural Network (DCLNN) and compared the model's accuracy with Nave Bayes and SVM classifiers.

In their research, the DCLNN shows the best result and has an average precision of 0.88 in four classes and 0.93 in two class, in the white blood cell classification.

III. MATERIAL AND METHODS

The key purpose of this study is to provide a CNN based model for processing white blood cells with the aim of classifying the type of these cells.

The flow chart of the overall proposed model stages is described in Figure 1.

A. Dataset Description

Kaggle white blood cells images were used in this research. This dataset comprises 12,444 augmented microscopic images of eosinophils, lymphocytes, monocytes, and neutrophils, with approximately 3,000 images for each of the four cell types [5]. The entire image is saved in JPEG format and has a pixel size of 320×240.

Figure 2 shows distribution of the blood cells in the dataset and in the figure 3 the WBC images in a sample view is shown



Figure 1. Proposed model stages.



Figure 2. The distribution of the blood cells in the dataset.



NEUTROPHIL

Figure 3. The WBC Image



B. Data Preprocessing

One of the most critical and required stages in machine learning is data preparation. This technique is essential for reliable, accurate, and successful prediction outcomes when using machine learning algorithms in a dataset.

In pre-process stage, at first, we rescale the photos to 120×120 to enhance the training speed of the proposed model, and because the Pixel values are presented in RGB images with integers between 0-255, we change the Pixel values to 0 and 1 to increase computational speed.

After pre-processing the images, we combined and shuffled all the white blood cell images and, we used for training as size of 80%, validation as size of 10%, and testing as size of 10% images.

The following is a general breakdown of the number of data samples:

The total number of training samples is 9955.

The total number of validation samples is 1245.

The total number of test samples is 1244.

C. Deep learning Methods and Algorithms used for Classification

The capacity to automatically extract visual characteristics using the idea of deep learning is very important advantage of convolutional neural networks (CNNs). As a result, it has become extremely popular in the medical area in recent years for diagnosing various illnesses.

In this article too, we built a CNN-based model for classifying white blood cell types. Figure 4 shows the proposed CNN-based model. This model is made up of five convolution blocks, which are responsible for extracting the features, flatten layer, fully connected layers and a final FC layer with SoftMax activation function.

Conv2D is used in the first convolution block, which is the input block, and SeparableConv2D (Separable convolutions) are used in the following convolution blocks. Each convolution block comprises two layers of convolution, followed by a 2×2 Max-Pooling filter. A 3×3 filter is used in all these blocks of convolution, and the number of neurons is 16, 32, 64, 128 and 256, respectively. In addition, each block has a batch normalization layer, except for the input block. A dropout layer with a value of 0.2 is employed in the third, fourth and fifth blocks of convolution to prevent overfitting.

The last convolution block's output is flattened using a flatten layer, then four Fully Connected (FC) layers are applied, each with its own Dropout layer. For multiclass classification, a final FC layer with four units and a SoftMax activation is implemented. The task of each layer in proposed CNN model shows in Table I.

Table I.The task of proposed CNN model layers [12].

Models Layers	Layer Task
Convolution Layer	Features Extraction in each block.
Pooling Layer	Reduce the number of parameters.
Batch Normalization	Normalize the output of convolution layers.
Dropout Layer	Prevent overfitting.
Flatten Layer	Flatten the output of last convolution block
Fully Connected layer	Perform mathematical operations and doing Classification with final FC layer.

In addition to the proposed model, this paper employed four pre-trained Keras models: MobileNetV2, DenseNet121, InceptionV3, and ResNet50. The most key characteristics of these models are listed in Table II.

Table II.

Models Key Characteristics [13,14]

Models	Number of Layers	Number of Trainable Parameters
MobileNetV2	53	3,504,872
DenseNet121	121	7,978,856
InceptionV3	48	23,817,352
ResNet50	50	25,583,592

The trainable parameter of the proposed model is 1,494,628, comparing with Table II. our proposed model has the lowest number of trainable parameters, which is mostly important in the model training phase.



Figure 4. The proposed CNN based model.

IV. EXPERIMENTAL RESULTS AND DISCUSSION

In this part of the article, the performance of the proposed model for classifying different types of white blood cells with different optimizers, including RMSprop, Adam, Adagrad and four pre-trained models such as MobileNetV2, DenseNet121, InceptionV3 and ResNet50, has been evaluated.

The Experimental studies in this project, performed on a work station with the following specifications: Intel Core i7, 2.30 GHz, GB Nvidia GeForce RTX 3060 graphics and 16 GB Ram memory.

We trained our proposed model by selecting the ReLU as an activation function in the convolution block, 32 Batch size, 0.000001 learning rate in 50 epochs, and evaluated its performance with RMSprop, Adam and Adagrad optimizers. In Figure 5, which shows the performance of the suggested model, with the three mentioned optimizers, the RMSprop optimizer with 99 percent train accuracy and 99 percent test accuracy provides the best result. The Adam optimizer produces the best results after the RMSprop optimizer, whereas the Adagrad optimizer produces the poorest results in the suggested model.

Optimizer RMSprop 0.9 Adam 0.8 Adagrad • 0.7 0.6 0.5 0.4 0.3 0.2 10 20 40 50 30 Epochs Test Accuracy Optimizer RMSprop 0.9 Adam 0.8 Adagrad 0.7 0.6 0.5 0.4 0.3 0.2 10 20 40 50 30

Figure 5. The performance of proposed model with three optimizers.

Epochs

Train Accuracy





Figure 6. The training & validation accuracy and loss curve.

Curves of training and test accuracy, as well as the curves of training and test loss with 50 epochs, are shown as in Figure 6. With increasing epochs, both training set and test set exhibit great accuracy. Simultaneously, the loss curves of training and test show a decrease in the loss ratio when the epochs are increased.

The confusion matrix in machine learning is a table that is used to display the performance of the algorithm. Accuracy, Precision, Recall, and F1-Score characteristics are used to evaluate the proposed approach's performance. The definitions and metrics for the confusion matrix parameters are listed in Table III.

Table III.

Confusion matrix parameters and metrics.

	Actual values		
	Positive (1)	Negative (0)	
Positive (1)	ТР	FP	
Occase Negative (0)	FN	TN	
Accuracy = $\frac{TP+T}{TP+TN+F}$	N P+FN	(1)	
$\operatorname{Recall} = \frac{TP}{TP + FN}$	(2)		
$Precision = \frac{TP}{TP + FP}$	(3)		
$F1\text{-score} = \frac{2*Recall*P}{Recall+Pr}$	(4)		

A atual values

TP- The forecasted value is positive, and it is right TN- The forecasted value is negative, and it is right FP - The forecasted value is positive, and it is wrong FN- The forecasted value is negative, and it is wrong The proposed model's confusion matrix is shown in Figure 7 The suggested model's accuracy, precision, recall, and F1 score are computed by using this matrix [15]. The confusion matrix shows that 307 photographs of eosinophils are properly predicted out of 314, all 299 photographs of lymphocytes and all 323 photographs of monocytes are successfully predicted, and 303 photographs of neutrophils are correctly predicted out of 308.



Figure 7. Confusion matrix of proposed CNN model.

Гable IV.	
Proposed Model Classification Result	

Class Name	Accuracy	Precision	Recall	F1 score
Eosinophils	99%	98%	98%	98%
Lymphocytes	100%	100%	100%	100%
Monocytes	100%	100%	100%	100%
Neutrophils	99%	98 %	98%	98 %
Overall	99.5%	99%	99%	99%



Table IV. shows the proposed model classification result which is computed according to confusion matrix of the model, in here we can see that the Lymphocytes and Monocytes images have been 100% correctly classified, and the overall accuracy of model is 99.5 %.

Table V.Different CNN Models Result.

CNN Models	Accuracy	Precision	Recall	F1 score	Training Time (Second)
CNN Based Proposed Model	99.5%	99%	99%	99%	10 min 52 sec
MobileNetV2	99.75%	100%	99.99%	100%	15 min 30 sec
DenseNet121	100%	100%	100%	100%	26 min 36 sec
InceptionV3	99.75%	99.93%	99.93	99.93	18 min 31 sec
ResNet50	99.99%	100%	100%	100%	21 min 30 sec

Table V. displays the results of the various CNN models used in this paper; we can see that all pretrained models have shown the best results, especially DenseNet121 with 100 percent accuracy, precision, recall, and F1.

According to Table II. and Table IV. It's worth to mention, that pre-trained models have extremely high trainable parameters, which increases the training time of the model. While our proposed CNN model with low number of trainable parameters and training time, among the mentioned models, shows considerable accuracy in classification of white blood cell, which is 99.5 %.

Table VI. compares the results of other research papers in the field of white blood cell classification with our paper.

Table VI.

The result comparisons of different research studies with our study.

Research Studies	Number of Classes	Methods	Accuracy
Cheque et al. [6]	4	Multi-level hybrid model, Faster R-CNN and MobileNet structure	98.4%
Çınar & Tuncer [7]	4	CNN Alexnet-Googlenet-SVM hybrid	99.73%
Akiz et al. [8]		Convolutional features and Support Vector Machines.	85.95%
Toğaçar et al. [9]	4	GoogLeNet, AlexNet, and ResNet-50 for feature extraction, and (QDA) for classification	97.95
Özyurt [10]		CNN-MRMR- ELM hybrid model	96.0.3 %
Tiwari et al. [11]	4	Double Convolution Layer Neural Network	An average precision of 0.88 in four classes and 0.93 in two class
Karthiyayini [16]	4	Fused convolutional neural network (CNN)	90.39%~90.79%
Jeyavathana and R. Balasubramanian [17]	5	CNN based Model	97%
Su et al. [18]	5	MLP	99.11%
		CNN Based Proposed Model	99.5%
		MobileNetV2	99.75%
This Paper	4	DenseNet121	100%
		InceptionV3	99.75%
		ResNet50	99.99%





Figure 8. Confusion matrix of Pre-trained CNN models.

V. CONCLUSION

White blood cells (WBCs) are a key element of the immune system and demonstrate resistance to a variety of illnesses, quantitative and qualitative examination of different kinds of WBCs is critical.

The main purpose of this study is to implement a CNN based model for processing of WBCs with the aim of classifying the type of these cells. We achieved this purpose by building a CNN-based model with low number of trainable parameters and training time for classification of white blood cell types and assessed the model's performance using several optimizers such as RMSprop, Adam, and Adagrad.

We have seen, that the RMSprop optimizer shows the best result in our proposed model. We have compared four pre-trained models such as MobileNetV2, DenseNet121, InceptionV3 and ResNet50 with our proposed model, that the DenseNet121 with 100 percent accuracy, precision, recall, and F1 score have shown the best result.

Compared to four pre-trained CNN models, and other related studies, our proposed model with the lowest number of trainable parameters and training time shows the great result with 99.5 percent accuracy, 99% recall, 99% precision, and 99% F1 score.

CONFLICTS OF INTEREST

There is no conflict of interest in this study.

RESEARCH AND PUBLICATION ETHICS

In the studies carried out within the scope of this article, the rules of research and publication ethics were followed.



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